

Q2
cont beta chain (SEQ ID NO:6; 32.7% identity over a 110 amino acid overlap), the human IL-9 receptor (SEQ ID NO:7; approximately 29.7% identity over a 158 amino acid overlap), and the murine IL-9 receptor (SEQ ID NO:8; approximately 28.3% identity over a 166 amino acid overlap) (see Figure 1A and 1B).

At page 13, line 25 through page 14, line 2, please replace the paragraph with the following:

Q3
090604-010423
The murine clone, m16445, encodes an approximately 2.5 Kb mRNA transcript having the corresponding cDNA set forth in SEQ ID NO:3. This transcript has a 1587 nucleotide open reading frame (nucleotides 391-1976 of SEQ ID NO:3), which encodes a 529 amino acid protein (SEQ ID NO:4) having a molecular weight of approximately 58.3 kDa. An analysis of the full-length m16445 polypeptide predicts that the N-terminal 19 amino acids represent a signal peptide. This polypeptide represents the protein sequence encoded by the murine orthologue of the h16445 gene. The mouse 16445 protein shares approximately 64.4% identity with the human 16445 protein disclosed in SEQ ID NO:2 (see Figure 1A and 1B).

At page 77, lines 4-25, please replace the two paragraphs with the following paragraphs:

Q4
090604-010423
The identified clone h16445 encodes a transcript of approximately 2.3 Kb (corresponding cDNA set forth in SEQ ID NO:1). The open reading frame (nt 349-1965) of this transcript encodes a predicted 538 amino acid protein (SEQ ID NO:2) having a molecular weight of approximately 59.1 kDa. A search of the nucleotide and protein databases revealed that h16445 encodes a precursor polypeptide that shares similarity with several cytokine receptor proteins. An alignment of the protein sequences having highest similarity to the h16445 precursor polypeptide is shown in Figure 1A and 1B. The alignment was generated using the Clustal method with PAM250 residue weight table and sequence identities were determined by FASTA (Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448).

The h16445 protein displays similarity to the human IL-2 receptor beta chain (approximately 36.9% over a 130 amino acid overlap; SEQ ID NO:5; SP Accession Number P14784; Hatakeyama *et al.* (1989) *Science* 244(4904):551-556). It also displays similarity to the murine IL-2 receptor beta chain (approximately 32.7% identity over a 110 amino acid overlap; SEQ ID NO:6; SP Accession Number P16297; Kono *et al.* (1990) *Proc. Natl. Acad. Sci. USA*